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 WIDEVIEW (TM)  
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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 on: Wed Aug 20 09:54:07 1997; MasPar time 12.22 Seconds  
 659,595 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-469-637A-2  
 Description: (22-401) from US08469637A.pep (2 of 2)  
 Perfect Score: 2861  
 Sequence: 1 ETRPPKYLHYDETSQQLC.....OKLEFMIGNQVOSVKISCL 380

Scoring table: PAM 150  
 Gap 11

Searched: 59021 seqs, 21210388 residues  
 Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:

Swiss-prot34  
 1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.034; Variance 81.732; scale 0.588

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

ult	No.	Score	Query Match	Length	ID	Description	Pred. No.
1	405	14.2	461	9	TNR2_HUMAN	TUMOR NECROSIS FACTOR	6,30e-63
2	375	13.1	474	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	5,56e-56
3	303	10.6	277	2	CD40_HUMAN	CD40L RECEPTOR PRECUR	2,64e-40
4	284	10.3	289	2	CD40_MOUSE	CD40L RECEPTOR PRECUR	2,31e-38
5	269	9.4	326	10	VT2_MYXL	LYMPHOTOXIN-BETA RECE	5,03e-33
6	265	9.3	415	9	TNR2_MOUSE	TUMOR NECROSIS FACTOR	3,52e-32
7	260	9.1	325	10	VT2_SFVKA	LYMPHOTOXIN-BETA RECE	3,98e-31
8	260	9.1	435	9	TNR2_HUMAN	LYMPHOTOXIN-BETA RECE	3,98e-31
9	230	8.0	349	10	VC22_VARY	PROTEIN C22/B28 HOMOL	6,59e-25
10	221	7.7	454	9	TNR1_MOUSE	TUMOR NECROSIS FACTOR	4,45e-23
11	220	7.7	461	9	TNR1_RAT	TUMOR NECROSIS FACTOR	7,09e-22
12	215	7.5	416	6	NGFR_CHICK	LOW-AFFINITY NERVE GR	7,20e-22
13	213	7.4	427	6	NGFR_HUMAN	LOW-AFFINITY NERVE GR	1,81e-21
14	207	7.2	425	6	NGFR_RAT	LOW-AFFINITY NERVE GR	2,85e-20
15	188	6.6	323	3	FASL_BOVIN	FASL RECEPTOR PRECURS	1,51e-16
16	186	6.5	461	9	TNR1_PIG	TUMOR NECROSIS FACTOR	3,67e-16
17	178	6.2	535	9	CD30_HUMAN	CD30L RECEPTOR PRECUR	1,67e-13
18	172	6.0	455	9	TNR1_HUMAN	TUMOR NECROSIS FACTOR	1,67e-13
19	159	5.6	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	4,22e-11
20	159	5.6	260	2	CD27_HUMAN	CD27L RECEPTOR PRECUR	4,22e-11
21	146	5.1	231	7	OX40_RAT	OX40L RECEPTOR PRECUR	8,91e-09
22	144	5.0	272	7	OX40_MOUSE	OX40L RECEPTOR PRECUR	2,00e-08

RESULT	1	STANDARD	PRT	461 AA.
ID	TNR2_HUMAN			
AC	P20333			
DT	01-FEB-1991 (REL. 17, CREATED)			
DI	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DE	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DT	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR			
DE	BINDING PROTEIN 2) (Tbpl1) (P80) (TNE-R2) (P75) (CD120B).			
GN	TNFR2 OR TNFR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90260639.			
RA	SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,			
RA	DOWER S.K., COSMAN D., GOODWIN R.G.,			
RL	SCIENCE 248:1019-1023(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91045991.			
RA	KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,			
RA	HALE K.K., SOUJRES C.H., THOMPSON R.C., VANNICE J.L.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).			
RN	[3]			
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE: 90349572.			
RA	HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,			
RA	RINDOLD G.M.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).			
RN	[4]			
RP	SEQUENCE OF 27-31.			
RX	MEDLINE: 90110215.			
RA	ENGELMANN H., NOVICK D., WALLACH D.,			
RA	J. BIOL. CHEM. 265:1531-1536(1990).			
RN	[5]			
RP	SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.			
RX	MEDLINE: 91056048.			
RA	LOETSCHER H., SCHLAGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,			
RA	BROCKHAUS M.,			
RL	J. BIOL. CHEM. 265:20131-20138(1990).			
RN	[6]			
RP	CHARACTERIZATION.			
RX	MEDLINE: 93016040.			
RA	PENNICIA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,			
RA	LIPARTI M.T., GOEDDEL D.V.,			

ALIGNMENTS

RESULT	1	STANDARD	PRT	461 AA.
ID	TNR2_HUMAN			
AC	P20333			
DT	01-FEB-1991 (REL. 17, CREATED)			
DI	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DE	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)			
DT	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR			
DE	BINDING PROTEIN 2) (Tbpl1) (P80) (TNE-R2) (P75) (CD120B).			
GN	TNFR2 OR TNFR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
NP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90260639.			
RA	SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,			
RA	DOWER S.K., COSMAN D., GOODWIN R.G.,			
RL	SCIENCE 248:1019-1023(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91045991.			
RA	KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,			
RA	HALE K.K., SOUJRES C.H., THOMPSON R.C., VANNICE J.L.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).			
RN	[3]			
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE: 90349572.			
RA	HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,			
RA	RINDOLD G.M.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).			
RN	[4]			
RP	SEQUENCE OF 27-31.			
RX	MEDLINE: 90110215.			
RA	ENGELMANN H., NOVICK D., WALLACH D.,			
RA	J. BIOL. CHEM. 265:1531-1536(1990).			
RN	[5]			
RP	SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.			
RX	MEDLINE: 91056048.			
RA	LOETSCHER H., SCHLAGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,			
RA	BROCKHAUS M.,			
RL	J. BIOL. CHEM. 265:20131-20138(1990).			
RN	[6]			
RP	CHARACTERIZATION.			
RX	MEDLINE: 93016040.			
RA	PENNICIA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,			
RA	LIPARTI M.T., GOEDDEL D.V.,			

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RL J. BIOL. CHEM. 267:21172-21178(1992).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC -1- APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M32315; G189186; -
DR EMBL: M35857; G339752; -
DR EMBL: M35944; G339758; -
DR PIR: A35356; A35356.
DR PIR: A36007; A36007.
DR PIR: A36475; A36475.
DR PIR: B35010; B35010.
DR PIR: A23666; A23666.
DR HSSP: P19438; 1TNR.
DR MIM: 191191; -.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
KW PHOSPHORYLATION.
FT CHAIN 1 22
FT DOMAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT DOMAIN 39 201 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 POTENTIAL.
FT CARBOHYD 193 193 POTENTIAL.
FT CONFLICT 141 141 R -> P (IN REF. 3).
FT CONFLICT 196 196 R -> M (IN REF. 1).
FT CONFLICT 363 363 A -> T (IN REF. 3).
SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;

Query Match 14.2%; Score 405; DB 9; Length 461;
Best Local Similarity 41.8%; Pred. No. 6,30e-63;
Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
CC EUTHERIA; RODENTIA.
RN (1)
RX SEQUENCE FROM N.A.
RX MEDLINE: 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDEL D.V.; GOEDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN (2)
RX SEQUENCE FROM N.A.
RX MEDLINE: 91246168.
RA GOODWIN R.G., ANDERSON D., JERRY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
CC MOL. CELL. BIOL. 11:3020-3026(1991).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M60469; G199828; -
DR EMBL: M59378; G202095; -
DR PIR: B38634; B38634.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR.
DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
KW SIGNAL.
FT CHAIN 1 22
FT DOMAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 289 474 POTENTIAL.
FT DOMAIN 39 203 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 4 X TNFR-CYS.
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 120 164 TNFR-CYS 2.
FT REPEAT 165 203 TNFR-CYS 3.
FT DISULFID 40 54 TNFR-CYS 4.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;

Query Match 13.1%; Score 375; DB 9; Length 474;
Best Local Similarity 41.5%; Pred. No. 3.56e-56;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

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FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	142	169	BY SIMILARITY.
FT	DISULFID	172	187	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	179	179	POTENTIAL.
SO	SEQUENCE	415 AA;	44956 MW; 3535D121 CIRC32;	

Query Match	9.3%;	Score 265;	DB 9;	Length 415;
Best Local Similarity	28.9%;	Pred. No. 3.59e-32;		
Matches	54;	Conservative	30;	Mismatches 92; Indels 11; Gaps 8

Db	52	epmhvdcscpcpggefifavcsisqdvckctcpnhsynehnhlstdqlrtpcdilvgf	110
QY	34	ETSHQLLDCRCPPTLYLKHCTAKMTVCAPCPDHYTDSWHTSDECLYCSPKCE-LQY	92
Db	111	eevpcscdtracrcqpgmascvylhncvycseerlvlpqpgaeavtdhmdtncv	170
QY	93	VK-OECNTHNRVKECEGR--YLEIE--FCLNHR-S-CPGEGV-VQAGTPERNIVK	143
Db	171	pckpghfngntsparcqphtrcicqglveaapqtsydtckrppepgamllaillsl	230
QY	144	RCPGFFSNESNSAPKPKRHNCVSFELLTLTKKNALHNDNCNSNSSTQKCGIDVLCE	203
Db	231	vlflflft 237	
QY	204	EAFRFA 210	

RESULT	7	STANDARD;	PRT;	325 AA.
ID	VT2_SEVKA			
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SOURCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROMA VIRUS (STRAIN KASZA) (SEV).			
OC	VIRIDE: DS-DNA ENVELOPED VIRUSES; POXYTRIDAE; CHORDOPOXVIRINAE;			
OC	LEPORIPVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RL	VIROLOGY 160:20-30(1987).			
CC	[2]			
CC	FUNCTION.			
CC	RX MEDLINE; 91207415.			
CC	RA SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
CC	MCFADEEN G., GOODMAN R.G.;			
CC	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-1- FUNCTION: BINDS TO TNF-ALPHA AND THEREBY DEAMPENING THE POTENTIAL			
CC	RACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; M17433; -. NOT ANNOTATED_CDS.			
DR	EMBL; A23727; E199408; -.			
DR	PIR; B43692; B43692.			
DR	HSSP; P19438; 11NR.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	CARBOHYD	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.



01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1 OR TNFR-1.  
 OS MUS MUSCULUS (MOUSE).  
 OC ENKARYOTA; METAPODA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91187885.  
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,  
 RA WONG G.H., CHEN E.Y., GOEDEL D.V.;  
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91246168.  
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,  
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.;  
 RA MOL. CELL. BIOL. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91285014.  
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,  
 RA GRAY P.W., FELDMANN M., FOXWELL B.M.J.;  
 RA EUR. J. IMMUNOL. 21:1649-1656(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=SPLEEN;  
 RX MEDLINE: 92039815.  
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;  
 RA IMMUNOGENETICS 34:338-340(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94245292.  
 RA BEBO B.F., LINTHICUM D.S.;  
 RA IMMUNOGENETICS 39:450-451(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93156721.  
 RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;  
 RA MOL. IMMUNOL. 30:165-175(1993).  
 CC - FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M66468; G199826; -;  
 DR EMBL: M83377; G202097; -;  
 DR EMBL: X59238; G53579; -;  
 DR EMBL: X51796; G54849; -;  
 DR EMBL: L26349; G430733; -;  
 DR EMBL: M88067; G202102; JOINED.  
 DR EMBL: M76656; G202102; JOINED.  
 DR EMBL: M76655; G202102; JOINED.  
 DR PIR: A38634; GOMSTI.  
 DR PIR: S16677; S16677.  
 DR PIR: S19021; S19021.  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR PROSITE: PS0017; DEATH\_DOMAIN.  
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT DOMAIN 22 212  
 FT TRANSMEM 213 235  
 FT DOMAIN 236 434  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99

FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 202 202  
 FT CONFLICT 394 394  
 SQ SEQUENCE 454 AA; 50129 MW; 486ECC09 CRC32;  
 Query Match 7.78; Score 221; DB 9; Length 454;  
 Best Local Similarity 33.14; Pred. No. 4,456-23;  
 Matches 48; Conservative 21; Mismatches 65; Indels 11; Gaps 9;  
 Db 49 yvshknsicctckhgylyvsdcpsgrdtvcecekgftfsgqyltgciscckctre 108  
 QY 31 YDEETHQLCDKCPPTLYLKQCTAK-WKTVCAPCPDHYTDSWHTSDCLCSPVCKE 89  
 Db 109 msqvelspcqdktvcgckengfgylysethfcvdcspcfng-tvltipcketqntcgn 167  
 QY 90 LQYVK-QECNRTNRYCECKES---RYL-EIEF-CLKHSCPPGFVQAGIPERNTVCK 143  
 Db 168 -chagfflresccvpcshckkneec 191  
 QY 144 RCPDGFSSNETSSKA-P-CRKATNC 166  
 RESULT 11  
 ID TNFR1\_RAT STANDARD; PRT; 461 AA.  
 AC P22934;  
 DT 01-AUG-1991 (REL. 19, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1 OR TNFR-1.  
 OS RATRUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAPODA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91090841.  
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,  
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;  
 RA DNA CELL. BIOL. 9:705-715(1990).  
 CC - FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M63122; G207362; -;  
 DR EMBL: B36555; B36555.  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR PROSITE: PS0017; DEATH\_DOMAIN.  
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 461  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 363 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117



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FT SIGNAL 1 28
FT CHAIN 29 427 NGF RECEPTOR.
FT DOMAIN 29 250 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 251 272 POTENTIAL.
FT DOMAIN 273 427 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 189 4 X TNFR-CYS.
FT REPEAT 31 65 TNFR-CYS 1.
FT REPEAT 66 107 TNFR-CYS 2.
FT REPEAT 108 147 TNFR-CYS 3.
FT REPEAT 148 189 TNFR-CYS 4.
FT DOMAIN 344 421 DEATH DOMAIN.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 64 BY SIMILARITY.
FT DISULFID 67 83 BY SIMILARITY.
FT DISULFID 86 99 BY SIMILARITY.
FT DISULFID 89 107 BY SIMILARITY.
FT DISULFID 109 122 BY SIMILARITY.
FT DISULFID 125 138 BY SIMILARITY.
FT DISULFID 128 146 BY SIMILARITY.
FT DISULFID 149 164 BY SIMILARITY.
FT DISULFID 167 180 BY SIMILARITY.
FT DISULFID 170 188 BY SIMILARITY.
FT DOMAIN 197 248 SER/THR-RICH.
FT CARBOHYD 60 60 POTENTIAL.
SQ SEQUENCE 427 AA: 45183 MW: EE2924BD CRC32:

Query Match 7.48; Score 213; DB 6; Length 427;
Best Local Similarity 34.9%; Pred. No. 1.81e-21;
Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5;

Db 44 ckacnlgevgagpcgan-qtvcpcldsvtfsdvatpckpcte-cvqlgmsapcve 101
Qy 41 CDKCPRGTYLKHCHTAKMKVCAPCPDHY-YTDSWHTSDCLYCSPVCKELQVQKQECNR 99
Db 102 addavcrcaaygygdeetgcrceacrcvcsqglvfscqdknvtvcecpdgtysdeanhv 161
Qy 100 THNRVCECKEGRL-EL-EGCLKHSRCPFGVQAGTPERNVCKRCRCPDGFSSNETSSK 157
Db 162 dpcldpctvc 170
Qy 158 APCRKHTNC 166

RESULT 14
ID NGFR_RAT STANDARD: PRT: 425 AA.
AC P07174;
NM 01-APR-1988 (REL. 07, CREATED)
RA 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
RL 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
RN NATURE 325:593-597(1987).
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
GN NGFR.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE: 87115859.
RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
RL NATURE 325:593-597(1987).
RN (2)
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 93077038.
RA METSIS M., TIMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;
RL GENE 121:247-254(1992).
RN (1)
RP FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC -1- BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

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CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: X05137; G56756; -.
DR EMBL: X61269; -. NOT_ANNOTATED_CDS.
DR PIR: A26431; A26431.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR_NGFR.
DR PROSITE: PS50017; DEATH_DOMAIN.
DR RECEPTOR: NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KM PHOSPHORYLATION; SIGNAL.
FT SIGNAL 1 29
FT CHAIN 30 425 NGF RECEPTOR.
FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 252 273 POTENTIAL.
FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 190 4 X TNFR-CYS.
FT REPEAT 32 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT REPEAT 109 148 TNFR-CYS 3.
FT REPEAT 149 190 TNFR-CYS 4.
FT DOMAIN 198 249 SER/THR-RICH.
FT DOMAIN 354 419 DEATH DOMAIN.
FT DISULFID 33 44 BY SIMILARITY.
FT DISULFID 45 58 BY SIMILARITY.
FT DISULFID 48 65 BY SIMILARITY.
FT DISULFID 68 84 BY SIMILARITY.
FT DISULFID 87 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT DISULFID 110 123 BY SIMILARITY.
FT DISULFID 126 139 BY SIMILARITY.
FT DISULFID 129 147 BY SIMILARITY.
FT DISULFID 150 165 BY SIMILARITY.
FT DISULFID 168 181 BY SIMILARITY.
FT DISULFID 171 189 BY SIMILARITY.
FT CARBOHYD 61 61 POTENTIAL.
SQ SEQUENCE 425 AA: 45432 MW: 7D78F258 CRC32:

Query Match 7.28; Score 207; DB 6; Length 425;
Best Local Similarity 33.3%; Pred. No. 2.85e-20;
Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;

Db 45 ckacnlgevgagpcgan-qtvcpcldsvtfsdvatpckpcte-clglgmsapcve 102
Qy 41 CDKCPRGTYLKHCHTAKMKVCAPCPDHY-YTDSWHTSDCLYCSPVCKELQVQKQECNR 99
Db 103 addavcrcaaygygdeetgcrceacrcvcsqglvfscqdknvtvcecpdgtysdeanhv 162
Qy 100 THNRVCECKEGRL-EL-EGCLKHSRCPFGVQAGTPERNVCKRCRCPDGFSSNETSSK 157
Db 163 dpcldpctvc 171
Qy 158 APCRKHTNC 166

RESULT 15
ID FAS_A_BOVIN STANDARD: PRT: 323 AA.
AC P51867;
NM 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE FAS RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 96226401.
RA YOO J., STONE R.T., BEATTIE C.W.;
RL DNA CELL BIOL. 15:227-234(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES
CC CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

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CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
DR EMBL: U04794; G1262193; -  
KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 323 FAST RECEPTOR.  
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 171 168 POTENTIAL.  
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 45 163 3 X TNFR-CYS.  
FT REPEAT 45 80 TNFR-CYS 1.  
FT REPEAT 81 124 TNFR-CYS 2.  
FT REPEAT 125 163 TNFR-CYS 3.  
FT DOMAIN 222 302 DEATH DOMAIN.  
SQ SEQUENCE 323 AA: 36445 MW: 36445 DA5A2A59 CRC32;

Query Match 6.68; Score 188; DB 3; Length 323;  
Best Local Similarity 35.78; Pred. NO. 1.51e-16;  
Matches 40; Conservative 17; Mismatches 49; Indels 6; Gaps 6;  
Db 53 hgfcgpcppgkxngdcxrdgdtpevcylseegneytdkshsdcklrcs-1cdeehgle 111  
OY 37 HOLLCDKCPGPTGLKQHCITAKMKTV-CAPCPD-HYTDSWHTSDECLYCSPVCKELQ-Y- 92  
Db 112 vegncttrntkcrcksnfscnspcehncpctcehngliekctpsntkck 163  
OY 93 VKQECNRTNHRVCECKEGRYLEIEFLKHSRCPG-GFGVYQAGTPERNTVCK 143

Search completed: Wed Aug 20 09:55:23 1997  
Job time : 76 secs.